AMENDMENTS TO THE SPECIFICATION

- Please replace the paragraph on page 10, line 20 through page 11, line 2, with the following paragraph:

FIGS. 1A-1R2 are a table of marker genes for bladder tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (bladder) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

- Please replace the paragraph on page 11, lines 3-13 with the following paragraph:

FIGS. 2A-2T2 are a table of marker genes for breast tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (breast) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column ("Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 11, lines 14-21 with the following paragraph:

FIGS. 3A-3Z2 are a table of marker genes for central nervous system (CNS) tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (CNS) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 11, line 25 through page 12, line 6 with the following paragraph:

FIGS. 4A-4S2 are a table of marker genes for colorectal tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (colorectal) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 12, lines 7-17 with the following paragraph:

FIGS. 5A-5M2 are a table of marker genes for leukemia. The second column of the table (entitled "Distinction") shows the type of tumor (leukemia) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 12, lines 18-28 with the following paragraph:

FIGS. 6A-6W2 are a table of marker genes for lung tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (lung) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 13, lines 1-11 with the following paragraph:

FIGS. 7A-7D3 are a table of marker genes for lymphoma tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (lymphoma) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 13, lines 12-22 with the following paragraph:

FIGS. 8A-8X2 are a table of marker genes for melanoma tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (melanoma) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 13, line 23 through page 14, line 4 with the following paragraph:

FIGS. 9A-9C3 are a table of marker genes for mesothelioma tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (mesothelioma) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 14, lines 5-15 with the following paragraph:

FIGS. 10A-10P2 are a table of marker genes for ovarian tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (ovarian) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 14, lines 16-26 with the following paragraph:

FIGS. 11A-11O2 are a table of marker genes for pancreatic tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (pancreatic) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 14, line 26 through page 15, line 8 with the following paragraph:

FIGS. 12A-12V2 are a table of marker genes for prostate tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (prostate) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 15, lines 9-19 with the following paragraph:

FIGS. 13A-13N2 are a table of marker genes for renal tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (renal) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 15, line 20 through page 16, line 2 with the following paragraph:

FIGS. 14A-14A3 are a table of marker genes for uterine tumor types. The second column of the table (entitled "Distinction") shows the type of tumor (uterine) for which the marker gene is specific. The third column (entitled "Distance") shows the signal-to-noise distance, which is an indication of the robustness of the marker; the larger the number, the more robust (specific) the marker. The fourth, fifth and sixth columns show the result of permutation tests which are indicators of the possibility that the marker would appear by chance. The seventh column (entitled "Feature") shows the designation assigned to that marker on the ~~Affymetrix~~ AFFYMETRIX® microarray used as described in the Examples. This designation corresponds to a ~~GenBank~~ GENBANK® Accession number for the corresponding gene. The eighth column (entitled "Desc.") provides descriptive information about the marker gene.

➢ Please replace the paragraph on page 19, line 25 through page 20, line 16 with the following paragraph:

The gene expression value measured or assessed is the numeric value obtained from an apparatus that can measure gene expression levels. Gene expression levels refer to the amount of expression of the gene expression product, as described herein. The values are raw values from the apparatus, or values that are optionally re-scaled, filtered and/or normalized. Such data is obtained, for example, from a ~~GeneChip®~~ GENECHIP® brand probe array or Microarray (Affymetrix, Inc.; U.S. Pat. Nos. 5,631,734, 5,874,219, 5,861,242, 5,858,659, 5,856,174, 5,843,655, 5,837,832, 5,834,758, 5,770,722, 5,770,456, 5,733,729, 5,556,752, all of which are incorporated herein by reference in their entirety), and the expression levels are calculated with software (e.g., ~~Affymetrix GENECHIP~~ the AFFYMETRIX® GENECHIP® software). For example, nucleic acids (e.g., mRNA or DNA) from a sample that has been subjected to particular stringency conditions hybridize to the probes on the chip. The nucleic acid to be analyzed (e.g., the target) is isolated, amplified and labeled with a detectable label, (e.g., ^{32}P or fluorescent label) prior to hybridization to the arrays. After hybridization, the arrays are inserted into a scanner that can detect patterns of hybridization. These patterns are detected by detecting the labeled target now attached to the microarray, e.g., if the target is fluorescently labeled, the hybridization data are collected as light emitted from the labeled groups. Since labeled targets hybridize, under appropriate stringency conditions known to one of skill in the art, specifically to complementary oligonucleotides contained in the microarray, and since the sequence and position of each oligonucleotide in the array are known, the identity of the target nucleic acid applied to the probe is determined.

➢ Please replace the paragraph on page 20, lines 17-27 with the following paragraph:

Quantitation of gene expression patterns from the hybridization of a labeled nucleic acid microarray can be performed by scanning the microarray to

measure the amount of hybridization at each position on the microarray with an ~~Affymetrix~~ AFFYMETRIX® scanner (Affymetrix Inc., Santa Clara, Calif.). For each stimulus a time series of nucleic acid levels (C={C1,C2,C3, . . . Cn}) and a corresponding time series of nucleic acid levels (M={M1,M2,M3, . . . Mn}) in control medium in the same experiment as the stimulus is obtained. Quantitative data is then analyzed. Hybridization analysis using microarray is only one method for obtaining gene expression values. Other methods for obtaining gene expression values known in the art or developed in the future can be used with the present invention. Once the gene expression values are determined, the sample can be classified.

- Please replace the paragraph on page 27, lines 11-20 with the following paragraph:

The present invention also features arrays, for example, microarrays that have a plurality of oligonucleotide probes involved in tumor development immobilized thereon. The oligonucleotide probe may be specific for one or more genes specific for a particular tumor or tumor class, selected from those genes described herein. Such genes can be obtained using their ~~GenBank~~ GENBANK® Accession Numbers identified in FIGS. 1A-1R2, FIGS. 2A-2T2, FIGS. 3A-3Z2, FIGS. 4A-4S2, FIGS. 5A-5M2, FIGS. 6A-6W2, FIGS. 7A-7D3, FIGS. 8A-8X2, FIGS. 9A-9C3, FIGS. 10A-10P2, FIGS. 11A-11O2, FIGS. 12A-12V2, FIGS. 13A-13N2, and FIGS. 14A-14A3. Methods for making oligonucleotide microarrays are well known in the art, and are described, for example, in WO 95/11995, the entire teachings of which are hereby incorporated by reference.

- Please replace the paragraph on page 28, lines 3-27 with the following paragraph:

Approximately 300 human tumor and normal tissue specimens were identified and obtained or purchased from a variety of academic or commercial sources. These specimens represented 30 individual classes of tumor or normal tissue with each class containing between 5 and 20 samples. Total RNA was

isolated from these specimens using standard laboratory protocols. "Target" (biotinylated) fragmented complementary RNA (cRNA) was produced from each sample using an established molecular biology protocol. Each Target was hybridized sequentially to two high density ~~Affymetrix~~ AFFYMETRIX® oligonucleotide microarrays (Hu6800FL and Hu35KsubA; Affymetrix, Inc., Santa Clara, Calif.), and gene expression profiles (patterns) were measured using a modified confocal laser scanner according to the manufacturer's instructions.